

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/660,434
Source: 1/F.116
Date Processed by STIC: 1/3/07

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 01/03/2007

PATENT APPLICATION: US/10/660,434

TIME: 16:41:39

Input Set : F:\7570.APP

Output Set: N:\CRF4\01032007\J660434.raw

3 <110> APPLICANT: GLINSKII, GUENNADI V.

5 <120> TITLE OF INVENTION: GENE SEGREGATION AND BIOLOGICAL SAMPLE CLASSIFICATION

METHODS

7 <130> FILE REFERENCE: 23543-07570US

9 <140> CURRENT APPLICATION NUMBER: 10/660,434

10 <141> CURRENT FILING DATE: 2003-09-10

12 <150> PRIOR APPLICATION NUMBER: 60/410,018

13 <151> PRIOR FILING DATE: 2002-09-10

15 <150> PRIOR APPLICATION NUMBER: 60/411,155

16 <151> PRIOR FILING DATE: 2002-09-16

18 <150> PRIOR APPLICATION NUMBER: 60/429,168

19 <151> PRIOR FILING DATE: 2002-11-25

21 <150> PRIOR APPLICATION NUMBER: 60/444,348

22 <151> PRIOR FILING DATE: 2003-01-31

24 <150> PRIOR APPLICATION NUMBER: 60/460,826

25 <151> PRIOR FILING DATE: 2003-04-03

27 <160> NUMBER OF SEQ ID NOS: 2340

29 <170> SOFTWARE: PatentIn version 3.3

31 <210> SEQ ID NO: 1

32 <211> LENGTH: 4716

33 <212> TYPE: DNA

34 <213> ORGANISM: Homo sapiens

36 <400> SEQUENCE: 1

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41 agggggagg ggggtcccaa cgcccaagcc ggagccagag acgcggagcc cgcgcgagcg 180

43 tcggagacag ggctccagg ctccgaagcg acagagccgg gccccggccg ctgccagggg 240

45 ccccgcccg ccccccaact ccacccacg tccctcctgc agcccagctc cgcccgcagc 300

47 cgccgcggac caggcaggcc cgcaccgccc ccatgatgtg cgaggtgatg cccaccatca 360

49 gcgaggatgg ccggcggggc tcggcgctgg gcccgacga ggcgggcggg gagctggagc 420

51 gcctcatggt cacgatgtc acggagcgcg agcgctgct ggagacgctg cgcgaggcac 480

53 aggacgggtt ggctacagcg cagctgcggc tgcgcgagct cggccacgag aaggactcgc 540

55 tgcagcgcca gctcagcat gcgctgcccc aggagtgtgc agctctgacg aaggagctga 600

57 acttatgtcg ggagcagctg ctggagaggg aggaagagat tgcagagctg aaggcggaac 660

59 ggaacaacac gcggctgtc ctggaacacc tggagtgcct ggtgtccagg cacgagaggt 720

61 cactgcgcat gaccgtggtg aagcgccagg cccagtcgcc ggggtggggtc tcctcggagg 780

63 tagaagtgtc caaagctcta aagtctctct tcgagcacca caaggccctg gatgagaagg 840

65 tccgggagcg gctgcggatg gcgctggagc gcgtggcagt gctcgaggag gagctggaac 900

67 tgagcaatca ggagactctg aaccttcgag aacagctgtc taggcggcgg tcagggtggtg 960

69 aagagccggg caaggatggg gatgggcaga ctcttgccaa tggcctgggt cctggcgggg 1020

71 attccaaccg gcgcacagca gagctggagg aggcctgga gcggcagcgc gccgaggtgt 1080

73 gccagctgcg ggagcgctg gcggtgctgt gccgtcagat gagccagctg gaggaggagt 1140

75 tgggcaccgc gcaccgtgag ctgggcaagg cagaggaagc caactccaag ctgcagcgcg 1200

77 acctcaagga ggcgctggcg cagcgggaag atatggagga gcggtattaca aactggaga 1260

see p. 6-7

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| 81 | agaacgagtt | agctagcaag | gagtcgttgt | atcggcagag | tgaagagaag | agccgtcagc | 1380 |
| 83 | tggccgagtg | gttggacgac | gccaagcaga | agctgcagca | gacgctgcag | aaagcggaga | 1440 |
| 85 | ccttgcccga | gatagaggcg | cagctggcgc | agcgctgggc | ggcgctcaac | aaggccgagg | 1500 |
| 87 | aacgtcatgg | gaattttgag | gagcggcttc | ggcagctgga | ggcccagctg | gaagagaaga | 1560 |
| 89 | atcaagagct | gcagcggggc | cggcagcggg | agaagatgaa | cgatgaccac | aataagcggc | 1620 |
| 91 | tgtccgagac | ggtggacaag | ctgctgagcg | agtccaacga | gcgcttacag | cttcacctca | 1680 |
| 93 | aggagcgcag | gggggcgctg | gaggagaaga | actccctgag | cgaggagata | gccaacatga | 1740 |
| 95 | agaagcttca | ggatgagttg | ctgctaaca | aggagcagct | cttggccgaa | atggagcggg | 1800 |
| 97 | tgcagatgga | gatcgaccag | ctgcggggga | ggccaccatc | ctcctactcc | aggtctctcc | 1860 |
| 99 | ctggcagtg | cctggagctc | cgttactctc | aggcaccac | tttaccttct | ggtgcccacc | 1920 |
| 101 | tggatcccta | tgtggctggc | agtggctcgg | caggcaagag | gggcccgtgg | tcaggggtca | 1980 |
| 103 | aggaggagcc | ctccaaggat | tgggagcggg | ctgcccctgc | gggctccata | ccacccccat | 2040 |
| 105 | tccctgggga | actggacggc | tccgatgagg | aggaggcaga | ggggatgttt | ggggccgagc | 2100 |
| 107 | tgtctgtccc | cagtgggcag | gctgacgtgc | agacgctggc | catcatgctt | caggagcagc | 2160 |
| 109 | tggaggccat | caacaaggag | atcaagctga | tccaagagga | gaaggagaca | acagaacaga | 2220 |
| 111 | gggcagagga | gctggagagt | cgggtgtcca | gctctggctt | ggactcgttg | ggccgctacc | 2280 |
| 113 | gcagcagctg | ctccctgccc | ccctccctca | ccacctctac | ccttgccagc | ccctccctcc | 2340 |
| 115 | ccagctctgg | ccactcaaca | ccccgcctga | caccccttag | ccctgcccgt | gagggcaccg | 2400 |
| 117 | acaaggctaa | tcatgtccct | aaggaggaag | ctggagctcc | acgaggggag | gggcccggca | 2460 |
| 119 | tcccaggaga | cacccaccca | cccactcccc | gctctgcccg | tcttgagaga | atgaccagg | 2520 |
| 121 | ccttggcact | gcaggcgggg | tccctggaag | atgggggacc | cccacgggga | agtgagggca | 2580 |
| 123 | ccccagattc | tctgcacaaa | gcccccaaga | agaagagcat | caagtcatcc | ataggccgtc | 2640 |
| 125 | tctttggcaa | gaaagagaag | ggacgaatgg | gacccccagg | ccgggacagc | tcttctctgg | 2700 |
| 127 | ctggaacacc | ctcagatgag | acactggcca | ctgacctctc | ggggctagcc | aagctgacag | 2760 |
| 129 | gcccaggaga | caaggaccga | aggaacaaga | ggaagcatga | actcctggag | gaggcctgcc | 2820 |
| 131 | gccagggcct | accttttgct | gcctgggacg | ggcccaccgt | ggtgtcctgg | ctggagctgt | 2880 |
| 133 | gggtgggcat | gcctgcctgg | tatgtggccg | cctgcccggc | caatgtcaag | agcggtgcca | 2940 |
| 135 | tcattggcaa | cctgtcagac | acggagatcc | agcgcgagat | cggcatcagc | aaccgcgtgc | 3000 |
| 137 | accgactcaa | gctacgcctc | gccatccagg | agatggtctc | gctcacctcg | ccctcagccc | 3060 |
| 139 | ccgcctcctc | ccgcacttcc | acaggaaacg | tgtggatgac | acacgaggag | atggagtccc | 3120 |
| 141 | ttacggccac | gaccaagccc | gagaccaagg | agatcagctg | ggagcagatc | ctggcatatg | 3180 |
| 143 | gcgacatgaa | ccacgagtgg | gtggggaacg | actggctgcc | cagcctgggg | ctgcccctaa | 3240 |
| 145 | accgcagcta | cttcatggag | tcgctggtgg | acgctcgaat | gttagatcac | cttaacaaga | 3300 |
| 147 | aggagctccg | gggccaactc | aagatggtgg | acagctttca | cagggtgagt | ctacattatg | 3360 |
| 149 | ggattatgtg | cctgaaacgg | ctcaactatg | accggaagga | cctggagcgg | aggcgggaag | 3420 |
| 151 | aaagtacagc | ccagatccga | gacgtgatgg | tgtggtccaa | tgagcgggtc | atgggttggg | 3480 |
| 153 | tgtccgggct | gggcctgaag | gaatttgcca | cgaacctcac | ggagagcggg | gtacacgggg | 3540 |
| 155 | cactgctcgc | cctggacgag | accttcgact | actccgacct | ggccttgctc | ctgcagatcc | 3600 |
| 157 | ccacgcagaa | tgcacaggcc | cggcagcttc | tggagaagga | attcagcaac | cttatctcct | 3660 |
| 159 | taggcacaga | caggcggctg | gacgaggaca | gcgccaagtc | tttcagccgc | tccccatcct | 3720 |
| 161 | ggcgggaagat | gttccgggag | aaggacctcc | gaggcgtaac | tcccgactca | gctgagatgt | 3780 |
| 163 | tgccccccaa | ctttcgctcg | gctgcagcgg | gagccctggg | ctctccgggg | ctccctctcc | 3840 |
| 165 | gcaagctgca | gccagaaggc | cagacttctg | ggagttcccg | ggcagacggc | gtttcggtcc | 3900 |
| 167 | ggacctatcc | ctgctagtgc | aggcctccag | gtgacctcac | tcggacggaa | gaatcttccc | 3960 |
| 169 | gaggctgggc | tgttccctct | cctgcccggg | ctgtggcctc | gccggggaga | gcgggcgggg | 4020 |
| 171 | gagctcgcgc | cgaggactgg | accatctgta | cagaccagcg | ggagtgcgcg | cgcccgcctc | 4080 |
| 173 | gcacagggcc | ggggcctgga | ccaaaccaca | tgaactggac | tgagaggggg | aagaagcggg | 4140 |
| 175 | gaggaagaaa | tcccgcccca | aacgtccgct | ttccttttct | ctactttgta | atttattgat | 4200 |

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177 cagtttctgt tgggagacgg gtgtccttta cccgcgggaa gggggcgggg cttccctccc 4260
179 gggccgcatg cggggagagg ctgtccctc ccctttttcc tgcccagtcg cggggcccaa 4320
181 gtcttccttc ttcgtccgaa aggaggggag gggggactcg ctgctacaag cctcgcccc 4380
183 tgtgccactc agctccgccc cgcgcgtcc ggtcgccgtt ccccggggtc atctgcgggc 4440
185 ggggtccctt ctccctcccc cgtgtctcgt gtccccgggg cctcaccgcc ccccggtctg 4500
187 tggccgtgtc cgtgccccgg gggtaggggg cgcagaatgg cgcttccctt tctcctctgg 4560
189 ctccgggggt tgcattggag aatcctcttt ccacgatgcc gctggggcag gtggcggtgg 4620
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197 <211> LENGTH: 1267
198 <212> TYPE: PRT
199 <213> ORGANISM: Homo sapiens
201 <400> SEQUENCE: 2
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203 1 5 10 15
206 Arg Gly Ala Arg Ala Ser Val Gly Asp Arg Ala Pro Gly Leu Arg Ser
207 20 25 30
210 Asp Arg Ala Gly Pro Arg Pro Leu Pro Gly Ala Pro Pro Gly Pro Pro
211 35 40 45
214 Thr Pro Pro His Val Pro Pro Ala Ala Gln Leu Arg Pro Gln Pro Pro
215 50 55 60
218 Arg Thr Arg Gln Ala Arg Thr Ala Ala Met Met Cys Glu Val Met Pro
219 65 70 75 80
222 Thr Ile Ser Glu Asp Gly Arg Arg Gly Ser Ala Leu Gly Pro Asp Glu
223 85 90 95
226 Ala Gly Gly Glu Leu Glu Arg Leu Met Val Thr Met Leu Thr Glu Arg
227 100 105 110
230 Glu Arg Leu Leu Glu Thr Leu Arg Glu Ala Gln Asp Gly Leu Ala Thr
231 115 120 125
234 Ala Gln Leu Arg Leu Arg Glu Leu Gly His Glu Lys Asp Ser Leu Gln
235 130 135 140
238 Arg Gln Leu Ser Ile Ala Leu Pro Gln Glu Phe Ala Ala Leu Thr Lys
239 145 150 155 160
242 Glu Leu Asn Leu Cys Arg Glu Gln Leu Leu Glu Arg Glu Glu Glu Ile
243 165 170 175
246 Ala Glu Leu Lys Ala Glu Arg Asn Asn Thr Arg Leu Leu Leu Glu His
247 180 185 190
250 Leu Glu Cys Leu Val Ser Arg His Glu Arg Ser Leu Arg Met Thr Val
251 195 200 205
254 Val Lys Arg Gln Ala Gln Ser Pro Gly Gly Val Ser Ser Glu Val Glu
255 210 215 220
258 Val Leu Lys Ala Leu Lys Ser Leu Phe Glu His His Lys Ala Leu Asp
259 225 230 235 240
262 Glu Lys Val Arg Glu Arg Leu Arg Met Ala Leu Glu Arg Val Ala Val
263 245 250 255
266 Leu Glu Glu Glu Leu Glu Leu Ser Asn Gln Glu Thr Leu Asn Leu Arg
267 260 265 270
270 Glu Gln Leu Ser Arg Arg Arg Ser Gly Leu Glu Glu Pro Gly Lys Asp

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274 Gly Asp Gly Gln Thr Leu Ala Asn Gly Leu Gly Pro Gly Gly Asp Ser
275          290          295          300
278 Asn Arg Arg Thr Ala Glu Leu Glu Glu Ala Leu Glu Arg Gln Arg Ala
279 305          310          315          320
282 Glu Val Cys Gln Leu Arg Glu Arg Leu Ala Val Leu Cys Arg Gln Met
283          325          330          335
286 Ser Gln Leu Glu Glu Glu Leu Gly Thr Ala His Arg Glu Leu Gly Lys
287          340          345          350
290 Ala Glu Glu Ala Asn Ser Lys Leu Gln Arg Asp Leu Lys Glu Ala Leu
291          355          360          365
294 Ala Gln Arg Glu Asp Met Glu Glu Arg Ile Thr Thr Leu Glu Lys Arg
295          370          375          380
298 Tyr Leu Ser Ala Gln Arg Glu Ala Thr Ser Leu His Asp Ala Asn Asp
299 385          390          395          400
302 Lys Leu Glu Asn Glu Leu Ala Ser Lys Glu Ser Leu Tyr Arg Gln Ser
303          405          410          415
306 Glu Glu Lys Ser Arg Gln Leu Ala Glu Trp Leu Asp Asp Ala Lys Gln
307          420          425          430
310 Lys Leu Gln Gln Thr Leu Gln Lys Ala Glu Thr Leu Pro Glu Ile Glu
311          435          440          445
314 Ala Gln Leu Ala Gln Arg Val Ala Ala Leu Asn Lys Ala Glu Glu Arg
315          450          455          460
318 His Gly Asn Phe Glu Glu Arg Leu Arg Gln Leu Glu Ala Gln Leu Glu
319 465          470          475          480
322 Glu Lys Asn Gln Glu Leu Gln Arg Ala Arg Gln Arg Glu Lys Met Asn
323          485          490          495
326 Asp Asp His Asn Lys Arg Leu Ser Glu Thr Val Asp Lys Leu Leu Ser
327          500          505          510
330 Glu Ser Asn Glu Arg Leu Gln Leu His Leu Lys Glu Arg Met Gly Ala
331          515          520          525
334 Leu Glu Glu Lys Asn Ser Leu Ser Glu Glu Ile Ala Asn Met Lys Lys
335          530          535          540
338 Leu Gln Asp Glu Leu Leu Asn Lys Glu Gln Leu Leu Ala Glu Met
339 545          550          555          560
342 Glu Arg Met Gln Met Glu Ile Asp Gln Leu Arg Gly Arg Pro Pro Ser
343          565          570          575
346 Ser Tyr Ser Arg Ser Leu Pro Gly Ser Ala Leu Glu Leu Arg Tyr Ser
347          580          585          590
350 Gln Ala Pro Thr Leu Pro Ser Gly Ala His Leu Asp Pro Tyr Val Ala
351          595          600          605
354 Gly Ser Gly Arg Ala Gly Lys Arg Gly Arg Trp Ser Gly Val Lys Glu
355          610          615          620
358 Glu Pro Ser Lys Asp Trp Glu Arg Ser Ala Pro Ala Gly Ser Ile Pro
359 625          630          635          640
362 Pro Pro Phe Pro Gly Glu Leu Asp Gly Ser Asp Glu Glu Glu Ala Glu
363          645          650          655
366 Gly Met Phe Gly Ala Glu Leu Leu Ser Pro Ser Gly Gln Ala Asp Val
367          660          665          670

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370 Gln Thr Leu Ala Ile Met Leu Gln Glu Gln Leu Glu Ala Ile Asn Lys
371      675      680      685
374 Glu Ile Lys Leu Ile Gln Glu Glu Lys Glu Thr Thr Glu Gln Arg Ala
375      690      695      700
378 Glu Glu Leu Glu Ser Arg Val Ser Ser Ser Gly Leu Asp Ser Leu Gly
379 705      710      715      720
382 Arg Tyr Arg Ser Ser Cys Ser Leu Pro Pro Ser Leu Thr Thr Ser Thr
383      725      730      735
386 Leu Ala Ser Pro Ser Pro Pro Ser Ser Gly His Ser Thr Pro Arg Leu
387      740      745      750
390 Ala Pro Pro Ser Pro Ala Arg Glu Gly Thr Asp Lys Ala Asn His Val
391      755      760      765
394 Pro Lys Glu Glu Ala Gly Ala Pro Arg Gly Glu Gly Pro Ala Ile Pro
395      770      775      780
398 Gly Asp Thr Pro Pro Pro Thr Pro Arg Ser Ala Arg Leu Glu Arg Met
399 785      790      795      800
402 Thr Gln Ala Leu Ala Leu Gln Ala Gly Ser Leu Glu Asp Gly Gly Pro
403      805      810      815
406 Pro Arg Gly Ser Glu Gly Thr Pro Asp Ser Leu His Lys Ala Pro Lys
407      820      825      830
410 Lys Lys Ser Ile Lys Ser Ser Ile Gly Arg Leu Phe Gly Lys Lys Glu
411      835      840      845
414 Lys Gly Arg Met Gly Pro Pro Gly Arg Asp Ser Ser Ser Leu Ala Gly
415      850      855      860
418 Thr Pro Ser Asp Glu Thr Leu Ala Thr Asp Pro Leu Gly Leu Ala Lys
419 865      870      875      880
422 Leu Thr Gly Pro Gly Asp Lys Asp Arg Arg Asn Lys Arg Lys His Glu
423      885      890      895
426 Leu Leu Glu Glu Ala Cys Arg Gln Gly Leu Pro Phe Ala Ala Trp Asp
427      900      905      910
430 Gly Pro Thr Val Val Ser Trp Leu Glu Leu Trp Val Gly Met Pro Ala
431      915      920      925
434 Trp Tyr Val Ala Ala Cys Arg Ala Asn Val Lys Ser Gly Ala Ile Met
435      930      935      940
438 Ala Asn Leu Ser Asp Thr Glu Ile Gln Arg Glu Ile Gly Ile Ser Asn
439 945      950      955      960
442 Pro Leu His Arg Leu Lys Leu Arg Leu Ala Ile Gln Glu Met Val Ser
443      965      970      975
446 Leu Thr Ser Pro Ser Ala Pro Ala Ser Ser Arg Thr Ser Thr Gly Asn
447      980      985      990
450 Val Trp Met Thr His Glu Glu Met Glu Ser Leu Thr Ala Thr Thr Lys
451      995      1000      1005
454 Pro Glu Thr Lys Glu Ile Ser Trp Glu Gln Ile Leu Ala Tyr Gly
455      1010      1015      1020
458 Asp Met Asn His Glu Trp Val Gly Asn Asp Trp Leu Pro Ser Leu
459      1025      1030      1035
462 Gly Leu Pro Gln Tyr Arg Ser Tyr Phe Met Glu Ser Leu Val Asp
463      1040      1045      1050
466 Ala Arg Met Leu Asp His Leu Asn Lys Lys Glu Leu Arg Gly Gln

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:66; N Pos. 2320,2321,2336,2351,2363,2413,2723,2724,2725,2726,3730
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VERIFICATION SUMMARY

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Input Set : F:\7570.APP

Output Set: N:\CRF4\01032007\J660434.raw

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 L:28916 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:232 after pos.:0
 M:341 Repeated in SeqNo=232
 L:29838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:241 after pos.:420
 L:38527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:310 after pos.:60
 L:41776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:334 after pos.:0
 M:341 Repeated in SeqNo=334
 L:41859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:335 after pos.:32
 L:43077 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:348 after pos.:0
 M:341 Repeated in SeqNo=348
 L:43160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:349 after pos.:32
 L:48433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:396 after pos.:0
 M:341 Repeated in SeqNo=396
 L:48513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:398 after pos.:32
 L:49089 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:403 after pos.:0
 M:341 Repeated in SeqNo=403
 L:49172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:404 after pos.:32
 L:49250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:405 after pos.:60
 L:53083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:424 after pos.:600
 L:61505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:514 after pos.:240
 L:61556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:515 after pos.:60
 M:341 Repeated in SeqNo=515
 L:61585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:516 after pos.:240
 L:61625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:517 after pos.:300
 M:341 Repeated in SeqNo=517
 L:61712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:521 after pos.:120
 M:341 Repeated in SeqNo=521
 L:61756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:523 after pos.:0
 L:61836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:525 after pos.:0
 M:341 Repeated in SeqNo=525
 L:61870 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:526 after pos.:60
 M:341 Repeated in SeqNo=526
 L:61953 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:527 after pos.:180
 M:341 Repeated in SeqNo=527
 L:62010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:529 after pos.:360
 M:341 Repeated in SeqNo=529
 L:62034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:530 after pos.:0
 M:341 Repeated in SeqNo=530
 L:62071 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:531 after pos.:240
 L:62122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:532 after pos.:60
 M:341 Repeated in SeqNo=532
 L:62151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:533 after pos.:240
 L:62191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:534 after pos.:300
 M:341 Repeated in SeqNo=534
 L:62255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:537 after pos.:120
 M:341 Repeated in SeqNo=537
 L:62372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:542 after pos.:240

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/660,434

DATE: 01/03/2007

TIME: 16:41:40

Input Set : F:\7570.APP

Output Set: N:\CRF4\01032007\J660434.raw

M:341 Repeated in SeqNo=542

L:62409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:543 after pos.:480